

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	2	"20030175711"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/04/03 13:18
L2	21	("0064533" "0081295" "4722840" "5071651" "5143726" "5334394" "5374426" "5580859" "5698424" "5739026" "5766602" "5770380" "5789245" "5792462" "5814482" "5871747" "5928647" "6004763" "6054312" "6231864" "6380364").PN.	US-PGPUB; USPAT	OR	OFF	2006/04/03 13:21
L3	1	"20020081295"	US-PGPUB	OR	OFF	2006/04/03 13:21
L4	1	"20020064533"	US-PGPUB	OR	OFF	2006/04/03 13:23
L5	9	("9211291" "9630523" "9731948" "9815631" "200032227") .did.	DERWENT	OR	OFF	2006/04/03 13:26
L6	8	("200059928" "200023955" "200162284" "200185208").did.	DERWENT	OR	OFF	2006/04/03 13:35
L7	1	2001-589796.NRAN.	DERWENT	OR	OFF	2006/04/03 13:28
L8	2	"20030086938".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/04/03 13:29
L9	2	"200023955".did.	DERWENT	OR	OFF	2006/04/03 13:40
L10	2	"9928478".did.	DERWENT	OR	OFF	2006/04/03 13:42
L11	45	1 2 3 4 5 6 7 8 9 10	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/04/03 13:42
L12	57156	amyloid alzheimer alzheimers	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/04/03 13:42
L13	8	11 and 12	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/04/03 13:43
L14	5	("0259149" "0385610" "9406472").did.	EPO; DERWENT	OR	OFF	2006/04/03 13:44
L15	26	("0259149" "0385610")".pn.."	EPO; DERWENT	OR	OFF	2006/04/03 13:45
L16	0	ep0259149	EPO; DERWENT	OR	OFF	2006/04/03 13:45

EAST Search History

L17	0	ep0259149.did.	EPO; \ DERWENT	OR	OFF	2006/04/03 13:45
L18	0	ep-0259149.did.	EPO; DERWENT	OR	OFF	2006/04/03 13:49
L19	1398863	partical or particle or vlp	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/04/03 13:49
L20	57171	amyloid or alzheimer	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/04/03 13:49
L21	146	19 with 20	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/04/03 13:50
L22	2006339	display	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/04/03 13:50
L23	398	20 with 22	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/04/03 13:50
L24	27	coat with 12	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/04/03 14:01
L25	4	"2003080665".did.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/04/03 14:01

? ds

Set	Items	Description
S1	1179659	DT=REVIEW?
S2	28113	AMYLOID
S3	4421	S1 AND S2
S4	92195	VACCINE
S5	23	S2(5N)S4
S6	7	S5 AND S1
S7	37518	CLINICAL(W)TRIAL
S8	34	S3 AND S7

? log hold

27mar06 13:47:39 User208669 Session D3010.2

\$6.73 1.981 DialUnits File155

\$0.00 41 Type(s) in Format 6

\$4.18 19 Type(s) in Format 7

\$4.18 60 Types

\$10.91 Estimated cost File155

\$2.40 TELNET

\$13.31 Estimated cost this search

\$13.72 Estimated total session cost 2.093 DialUnits

Logoff: level 05.10.03 D 13:47:39

? ds

Set	Items	Description
S1	51	AU=SCHILLER? AND SELF
S2	11	AU=LOWY? AND S1

? log hold

03apr06 14:04:59 User208669 Session D3014.2

\$2.07 0.610 DialUnits File155

\$0.00 11 Type(s) in Format 6

\$0.44 2 Type(s) in Format 7

\$0.44 13 Types

\$2.51 Estimated cost File155

\$2.13 TELNET

\$4.64 Estimated cost this search

\$5.07 Estimated total session cost 0.728 DialUnits

Logoff: level 05.11.04 D 14:04:59

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 24, 2006, 12:13:22 ; Search time 167 Seconds
(without alignments)
45.035 Million cell updates/sec

Title: US-10-050-898A-367
Perfect score: 108
Sequence: 1 DAEFRHDSGYEVHHQGGC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match	Length	DB	ID	Description
	Score	Match					
1	108	100.0	18	4	US-10-617-876-8	Sequence 8, Appli	
2	92	85.2	30	4	US-10-617-876-9	Sequence 9, Appli	
3	87	80.6	15	5	US-10-810-881A-92	Sequence 92, Appl	
4	87	80.6	15	5	US-10-810-881A-102	Sequence 102, App	
5	87	80.6	15	5	US-10-625-854-12	Sequence 12, Appl	
6	87	80.6	16	3	US-09-155-076-2	Sequence 2, Appli	
7	87	80.6	16	4	US-10-411-544-22	Sequence 22, Appl	
8	87	80.6	16	4	US-10-423-047-2	Sequence 2, Appli	
9	87	80.6	16	5	US-10-625-854-13	Sequence 13, Appl	
10	87	80.6	17	3	US-09-992-800-2	Sequence 2, Appli	
11	87	80.6	17	3	US-09-992-994-2	Sequence 2, Appli	

12	87	80.6	17	3	US-09-930-915A-188	Sequence 188, App
13	87	80.6	17	4	US-10-082-014-82	Sequence 82, Appl
14	87	80.6	17	4	US-10-372-076-83	Sequence 83, Appl
15	87	80.6	17	4	US-10-385-065-2	Sequence 2, Appli
16	87	80.6	17	4	US-10-732-862A-96	Sequence 96, Appl
17	87	80.6	17	4	US-10-806-006-188	Sequence 188, App
18	87	80.6	17	4	US-10-677-074-83	Sequence 83, Appl
19	87	80.6	17	4	US-10-805-913-188	Sequence 188, App
20	87	80.6	17	6	US-11-063-350-2	Sequence 2, Appli
21	87	80.6	18	3	US-09-792-079-3	Sequence 3, Appli
22	87	80.6	18	4	US-10-159-279-3	Sequence 3, Appli
23	87	80.6	19	3	US-09-792-079-4	Sequence 4, Appli
24	87	80.6	19	4	US-10-159-279-4	Sequence 4, Appli
25	87	80.6	20	3	US-09-792-079-6	Sequence 6, Appli
26	87	80.6	20	4	US-10-159-279-6	Sequence 6, Appli
27	87	80.6	28	3	US-09-867-847-4	Sequence 4, Appli
28	87	80.6	28	3	US-09-865-294-66	Sequence 66, Appl
29	87	80.6	28	3	US-09-792-079-5	Sequence 5, Appli
30	87	80.6	28	4	US-10-159-279-5	Sequence 5, Appli
31	87	80.6	28	4	US-10-363-082-2	Sequence 2, Appli
32	87	80.6	28	4	US-10-433-385-7	Sequence 7, Appli
33	87	80.6	28	4	US-10-390-472-4	Sequence 4, Appli
34	87	80.6	28	4	US-10-250-581-2	Sequence 2, Appli
35	87	80.6	28	4	US-10-250-581-5	Sequence 5, Appli
36	87	80.6	28	4	US-10-250-581-8	Sequence 8, Appli
37	87	80.6	28	4	US-10-250-581-11	Sequence 11, Appl
38	87	80.6	28	4	US-10-250-581-14	Sequence 14, Appl
39	87	80.6	28	4	US-10-250-581-17	Sequence 17, Appl
40	87	80.6	28	4	US-10-741-205-36	Sequence 36, Appl
41	87	80.6	28	4	US-10-416-262B-7	Sequence 7, Appli
42	87	80.6	28	4	US-10-478-308-4	Sequence 4, Appli
43	87	80.6	28	4	US-10-478-307-4	Sequence 4, Appli
44	87	80.6	28	5	US-10-861-614-66	Sequence 66, Appl
45	87	80.6	28	5	US-10-825-958-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
 US-10-617-876-8
 ; Sequence 8, Application US/10617876
 ; Publication No. US20040076611A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bachmann, Martin F
 ; APPLICANT: Tissot, Alain
 ; APPLICANT: Pumpens, Paul
 ; APPLICANT: Cielens, Indulis
 ; APPLICANT: Renhofa, Regina
 ; TITLE OF INVENTION: Molecular Antigen Arrays
 ; FILE REFERENCE: 1700.0310001
 ; CURRENT APPLICATION NUMBER: US/10/617,876
 ; CURRENT FILING DATE: 2003-07-14
 ; PRIOR APPLICATION NUMBER: US 60/396,126
 ; PRIOR FILING DATE: 2002-07-17
 ; NUMBER OF SEQ ID NOS: 125
 ; SOFTWARE: PatentIn version 3.2

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 24, 2006, 12:12:42 ; Search time 47 Seconds
 (without alignments)
 31.663 Million cell updates/sec

Title: US-10-050-898A-367
 Perfect score: 108
 Sequence: 1 DAEFRHDSGYEVHHQGGC 18

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents AA:*
 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%				
Result		Query				
No.	Score	Match	Length	DB	ID	Description
1	87	80.6	15	1	US-08-609-090-1	Sequence 1, Appli
2	87	80.6	16	1	US-08-302-808-10	Sequence 10, Appl
3	87	80.6	16	1	US-08-986-948-10	Sequence 10, Appl
4	87	80.6	17	2	US-09-594-366-2	Sequence 2, Appli
5	87	80.6	17	2	US-09-992-800-2	Sequence 2, Appli
6	87	80.6	21	1	US-08-659-984A-18	Sequence 18, Appl
7	87	80.6	21	2	US-08-660-531-18	Sequence 18, Appl
8	87	80.6	21	2	US-09-404-578-18	Sequence 18, Appl
9	87	80.6	27	1	US-08-141-324-11	Sequence 11, Appl
10	87	80.6	27	1	US-08-141-324-12	Sequence 12, Appl
11	87	80.6	27	1	US-08-541-902-11	Sequence 11, Appl

12	87	80.6	27	1	US-08-541-902-12	Sequence 12, Appl
13	87	80.6	28	1	US-08-346-849-4	Sequence 4, Appli
14	87	80.6	28	1	US-08-302-808-7	Sequence 7, Appli
15	87	80.6	28	1	US-08-609-090-2	Sequence 2, Appli
16	87	80.6	28	1	US-08-986-948-7	Sequence 7, Appli
17	87	80.6	28	1	US-08-293-284A-4	Sequence 4, Appli
18	87	80.6	28	1	US-08-461-216-2	Sequence 2, Appli
19	87	80.6	28	2	US-09-388-890-2	Sequence 2, Appli
20	87	80.6	28	2	US-09-388-890-11	Sequence 11, Appl
21	87	80.6	28	2	US-09-388-890-12	Sequence 12, Appl
22	87	80.6	28	2	US-09-388-890-13	Sequence 13, Appl
23	87	80.6	28	2	US-09-388-890-14	Sequence 14, Appl
24	87	80.6	28	2	US-08-723-661B-2	Sequence 2, Appli
25	87	80.6	28	2	US-09-660-954-2	Sequence 2, Appli
26	87	80.6	28	2	US-09-660-954-11	Sequence 11, Appl
27	87	80.6	28	2	US-09-660-954-12	Sequence 12, Appl
28	87	80.6	28	2	US-09-660-954-13	Sequence 13, Appl
29	87	80.6	28	2	US-09-660-954-14	Sequence 14, Appl
30	87	80.6	28	2	US-08-898-300-4	Sequence 4, Appli
31	87	80.6	28	2	US-08-824-513-4	Sequence 4, Appli
32	87	80.6	28	2	US-09-623-548A-959	Sequence 959, App
33	87	80.6	28	2	US-09-623-548A-965	Sequence 965, App
34	87	80.6	28	2	US-09-623-548A-992	Sequence 992, App
35	87	80.6	28	2	US-09-657-276-959	Sequence 959, App
36	87	80.6	28	2	US-09-657-276-965	Sequence 965, App
37	87	80.6	28	2	US-09-657-276-992	Sequence 992, App
38	87	80.6	28	2	US-09-865-294A-66	Sequence 66, Appl
39	87	80.6	30	1	US-08-609-090-3	Sequence 3, Appli
40	87	80.6	30	2	US-09-861-847A-1	Sequence 1, Appli
41	87	80.6	30	2	US-09-861-847A-12	Sequence 12, Appl
42	87	80.6	30	2	US-09-861-847A-13	Sequence 13, Appl
43	87	80.6	30	2	US-09-861-847A-15	Sequence 15, Appl
44	87	80.6	33	1	US-08-609-090-4	Sequence 4, Appli
45	87	80.6	33	1	US-08-659-984A-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1

US-08-609-090-1

; Sequence 1, Application US/08609090

; Patent No. 5840838

; GENERAL INFORMATION:

; APPLICANT: HENSLEY, Kenneth

; APPLICANT: BUTTERFIELD, D. A.

; APPLICANT: CARNEY, John M.

; APPLICANT: AKSENOV, Michael

; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF

; TITLE OF INVENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LOWE PRICE LEBLANC & BECKER

; STREET: 99 Canal Center Plaza, Suite 300

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: USA

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OM protein - protein search, using sw model

Run on: March 24, 2006, 12:05:13 ; Search time 190 Seconds
(without alignments)
41.625 Million cell updates/sec

Title: US-10-050-898A-367
Perfect score: 108
Sequence: 1 DAEFRHDSGYEVHHQGGC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	108	100.0	18	5	ABG80708	Abg80708 Modified
2	108	100.0	18	5	ABG80715	Abg80715 Human IgG
3	108	100.0	18	5	ABG80703	Abg80703 Modified
4	108	100.0	18	8	ADI40717	Adi40717 Abeta 1-1
5	92	85.2	30	5	ABG94392	Abg94392 A beta pe
6	92	85.2	30	5	ABG80717	Abg80717 Mouse Res
7	92	85.2	30	5	ABG80704	Abg80704 Modified
8	92	85.2	30	8	ADI40718	Adi40718 Abeta 1-2

9	87	80.6	15	2	AAW81466	Aaw81466	Synthetic
10	87	80.6	15	8	ADJ71349	Adj71349	N-termina
11	87	80.6	15	9	ADZ08877	Adz08877	Human bet
12	87	80.6	15	9	ADZ08867	Adz08867	Human bet
13	87	80.6	16	2	AAR60371	Aar60371	Beta-amyl
14	87	80.6	16	2	AAW35344	Aaw35344	Human bet
15	87	80.6	16	2	AAY49693	Aay49693	Human bet
16	87	80.6	16	5	ABB81322	Abb81322	Amyloid p
17	87	80.6	16	7	ADM80641	Adm80641	Human pep
18	87	80.6	16	8	ADJ71350	Adj71350	N-termina
19	87	80.6	16	9	ADW88082	Adw88082	T668 phos
20	87	80.6	16	9	ADX44529	Adx44529	Human APP
21	87	80.6	16	9	ADZ20481	Adz20481	Amyloid b
22	87	80.6	17	3	AAB11496	Aab11496	Human amy
23	87	80.6	17	4	AAB48345	Aab48345	Beta-amyl
24	87	80.6	17	5	AAU93920	Aau93920	Human bet
25	87	80.6	17	7	ADE10849	Adel0849	Chimeric
26	87	80.6	17	7	ADM39754	Adm39754	B-cell pe
27	87	80.6	17	8	ADG63949	Adg63949	Recombina
28	87	80.6	17	8	ADP73483	Adp73483	Alzheimer
29	87	80.6	17	8	ADR12776	Adr12776	Human bet
30	87	80.6	18	6	ABU63710	Abu63710	Rat amylo
31	87	80.6	18	7	ADF55639	Adf55639	Human A b
32	87	80.6	19	6	ABU63711	Abu63711	Rat amylo
33	87	80.6	19	7	ADF55640	Adf55640	Human A b
34	87	80.6	20	6	ABU63713	Abu63713	Rat amylo
35	87	80.6	20	7	ADF55642	Adf55642	Human A b
36	87	80.6	21	2	AAW08361	Aaw08361	Beta-secr
37	87	80.6	21	2	AAY30942	Aay30942	Human sec
38	87	80.6	21	2	AAY33755	Aay33755	Synthetic
39	87	80.6	21	4	AAB47265	Aab47265	Peptide 5
40	87	80.6	21	8	ADU24439	Adu24439	Novel glu
41	87	80.6	21	8	ADU46713	Adu46713	Amyloid b
42	87	80.6	21	9	ADV86872	Adv86872	Beta-amyl
43	87	80.6	21	9	ADX44523	Adx44523	Human APP
44	87	80.6	21	9	ADZ71365	Adz71365	Human bet
45	87	80.6	21	9	AEA35398	Aea35398	Novel QC

ALIGNMENTS

RESULT 1

ABG80708

ID ABG80708 standard; peptide; 18 AA.

XX

AC ABG80708;

XX

DT 29-NOV-2002 (first entry)

XX

DE Modified human amyloid beta peptide Abeta 1-15 #2.

XX

KW Molecular antigen array; vaccine; antigen; antimicrobial; mutant;

KW molecular scaffold; amyloid beta; Abeta 1-42; influenza; mutein;

KW graft versus host disease; IgE-mediated allergic reaction; anaphylaxis;

KW adult respiratory distress syndrome; ARDS; Crohn's disease;

KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;

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OM protein - protein search, using sw model

Run on: March 24, 2006, 12:05:18 ; Search time 229 Seconds
(without alignments)
55.456 Million cell updates/sec

Title: US-10-050-898A-367
Perfect score: 108
Sequence: 1 DAEFRHDSGYEVHHQGGC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	87	80.6	33	2	Q9UC33_HUMAN	Q9uc33	homo sapien
2	87	80.6	42	2	Q56JJ6_GRAGR	Q56jj6	grampus gri
3	87	80.6	42	2	Q56JJ7_TURTR	Q56jj7	tursiops tr
4	87	80.6	42	2	Q7M088_CAVPO	Q7m088	cavia porce
5	87	80.6	57	1	A4_URSMA	Q29149	u alzheimer
6	87	80.6	58	1	A4_CANFA	Q28280	c alzheimer
7	87	80.6	58	1	A4_RABIT	Q28748	o alzheimer
8	87	80.6	58	1	A4_SHEEP	Q28757	o alzheimer
9	87	80.6	59	1	A4_BOVIN	Q28053	b alzheimer
10	87	80.6	113	2	Q8JH58_CHESE	Q8jh58	chelydra se
11	87	80.6	534	2	O93296_CHICK	O93296	gallus gall
12	87	80.6	569	2	Q9PVL1_CHICK	Q9pvl1	gallus gall
13	87	80.6	695	2	Q5R477_PONPY	Q5r477	pongo pygma
14	87	80.6	695	2	Q6RH29_CANFA	Q6rh29	canis famil
15	87	80.6	695	2	Q56JK3_CANFA	Q56jk3	canis famil

16	87	80.6	695	2	Q9DGJ8_CHICK	Q9dgj8	gallus	gall
17	87	80.6	714	2	Q56JK4_CANFA	Q56jk4	canis	famil
18	87	80.6	749	2	Q56JK2_STECO	Q56jk2	stenella	co
19	87	80.6	751	1	A4_SAIISC	Q95241	s	amyloid b
20	87	80.6	751	2	Q6GSC0_HUMAN	Q6gsc0	homo	sapien
21	87	80.6	751	2	Q6RH28_CANFA	Q6rh28	canis	famil
22	87	80.6	751	2	Q56JK5_CANFA	Q56jk5	canis	famil
23	87	80.6	751	2	Q4R4R8_MACFA	Q4r4r8	macaca	fasc
24	87	80.6	751	2	Q9DGJ7_CHICK	Q9dgj7	gallus	gall
25	87	80.6	770	1	A4_CAVPO	Q60495	c	amyloid b
26	87	80.6	770	1	A4_HUMAN	P05067	h	amyloid b
27	87	80.6	770	1	A4_MACFA	P53601	m	amyloid b
28	87	80.6	770	1	A4_PANTR	Q5is80	p	amyloid b
29	87	80.6	770	1	A4_PIG	P79307	s	amyloid b
30	87	80.6	770	2	Q6RH30_CANFA	Q6rh30	canis	famil
31	87	80.6	770	2	Q56JK6_CANFA	Q56jk6	canis	famil
32	82	75.9	52	2	Q8WZ99_HUMAN	Q8wz99	homo	sapien
33	72	66.7	693	2	Q98SG0_XENLA	Q98sg0	xenopus	lae
34	72	66.7	695	2	Q98SF9_XENLA	Q98sf9	xenopus	lae
35	72	66.7	695	2	Q7ZXQ0_XENLA	Q7zxq0	xenopus	lae
36	72	66.7	747	2	Q91963_9PIPI	Q91963	xenopus.	ap
37	72	66.7	749	2	Q6NRR1_XENLA	Q6nrr1	xenopus	lae
38	72	66.7	750	2	Q6DJB6_XENTR	Q6djb6	xenopus	tro
39	68	63.0	79	2	O35463_CRIGR	O35463	cricetulus	
40	68	63.0	218	2	Q8BPV5_MOUSE	Q8bpv5	mus	musculu
41	68	63.0	384	2	Q8BPC7_MOUSE	Q8bpc7	mus	musculu
42	68	63.0	695	2	Q6GR78_MOUSE	Q6gr78	mus	musculu
43	68	63.0	733	2	Q6P6Q5_RAT	Q6p6q5	rattus	norv
44	68	63.0	770	1	A4_MOUSE	P12023	m	amyloid b
45	68	63.0	770	1	A4_RAT	P08592	r	amyloid b

ALIGNMENTS

RESULT 1

Q9UC33_HUMAN

ID Q9UC33_HUMAN PRELIMINARY; PRT; 33 AA.
AC Q9UC33;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-amyloid peptide (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93024877; PubMed=1406936; DOI=10.1038/359325a0;
RA Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D.,
RA Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.;
RT "Isolation and quantification of soluble Alzheimer's beta-peptide from
RT biological fluids.";
RL Nature 359:325-327(1992).
DR HSSP; Q16019; 1BA4.

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 24, 2006, 12:08:47 ; Search time 38 Seconds
 (without alignments)
 45.576 Million cell updates/sec

Title: US-10-050-898A-367
 Perfect score: 108
 Sequence: 1 DAEFRHDSGYEVHHQGGC 18

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR 80:*
 1: pirl:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					Description
Result	Query	Match	Length	DB	ID		
No.	Score						
1	87	80.6	42	2	PN0512		beta-amyloid prote
2	87	80.6	57	2	A60045		Alzheimer's diseas
3	87	80.6	57	2	F60045		Alzheimer's diseas
4	87	80.6	57	2	D60045		Alzheimer's diseas
5	87	80.6	57	2	E60045		Alzheimer's diseas
6	87	80.6	57	2	G60045		Alzheimer's diseas
7	87	80.6	57	2	B60045		Alzheimer's diseas
8	87	80.6	82	2	PQ0438		Alzheimer's diseas
9	87	80.6	695	1	A49795		Alzheimer's diseas
10	87	80.6	770	1	QRHUA4		Alzheimer's diseas
11	72	66.7	747	2	JH0773		Alzheimer's diseas
12	68	63.0	33	2	S23094		beta-amyloid prote
13	68	63.0	695	2	A27485		Alzheimer's diseas

14	68	63.0	695	2	S00550	Alzheimer's diseas
15	54	50.0	311	2	AF1266	L-lactate dehydrog
16	54	50.0	311	2	AH1628	L-lactate dehydrog
17	51.5	47.7	313	2	JT0960	polyprotein - pota
18	51.5	47.7	427	2	JA0073	genome polyprotein
19	50.5	46.8	284	2	S04723	genome polyprotein
20	50.5	46.8	327	2	S11435	genome polyprotein
21	50.5	46.8	519	2	PC1072	nuclear inclusion
22	50.5	46.8	1555	2	JT0959	polyprotein - pota
23	49	45.4	155	2	JC7732	trypsin-plasmin in
24	48.5	44.9	330	2	A26205	coat protein precu
25	48.5	44.9	3063	2	JS0166	genome polyprotein
26	48	44.4	274	2	A64978	hypothetical prote
27	48	44.4	473	1	T40391	phosphoprotein pho
28	48	44.4	526	1	T45058	phosphoprotein pho
29	46.5	43.1	971	2	D70128	conserved hypothet
30	46	42.6	113	2	A64064	ferredoxin [2Fe-2S
31	46	42.6	326	2	T16841	hypothetical prote
32	46	42.6	363	2	T16831	hypothetical prote
33	46	42.6	372	2	G90983	GDP-D-mannose dehy
34	46	42.6	372	2	B85829	GDP-mannose dehydr
35	46	42.6	392	2	T19869	hypothetical prote
36	46	42.6	403	2	S07825	hypothetical prote
37	46	42.6	984	2	S14382	hypothetical prote
38	45.5	42.1	379	2	S13556	genome polyprotein
39	45.5	42.1	3061	1	JN0545	genome polyprotein
40	45	41.7	337	2	F98335	adhesin, probable
41	45	41.7	337	2	AD2947	ABC transporter, s
42	45	41.7	475	2	G70958	hypothetical prote
43	45	41.7	489	2	AD2834	hypothetical prote
44	45	41.7	508	2	H97611	hypothetical prote
45	45	41.7	894	2	T20625	hypothetical prote

ALIGNMENTS

RESULT 1

PN0512

beta-amyloid protein - guinea pig (fragment)

C;Species: Cavia porcellus (guinea pig)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C;Accession: PN0512

R;Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno, M.

Biochem. Biophys. Res. Commun. 193, 624-630, 1993

A;Title: Receptor-mediated specific biological activity of a beta-amyloid protein fragment for NK-1 substance p receptors.

A;Reference number: PN0512; MUID:93290653; PMID:7685598

A;Accession: PN0512

A;Molecule type: protein

A;Residues: 1-42 <SHI>

A;Cross-references: UNIPROT:Q7M088; UNIPARC:UPI00000315E8

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

C;Keywords: alternative splicing; amyloid